

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/509,073C
Source: JE/016
Date Processed by STIC: 4/16/07

ENTERED



IFW16

RAW SEQUENCE LISTING

DATE: 04/16/2007

PATENT APPLICATION: US/10/509,073C

TIME: 18:45:57

Input Set : A:\Tsuneoka 2004_1597A.txt

Output Set: N:\CRF4\04162007\J509073C.raw

```

4 <110> APPLICANT: TSUNEOKA, Makoto
5   KIMURA, Hiroshi
7 <120> TITLE OF INVENTION: Cancer-Associated Gene Mina53, Protein Mina53
8   and Monoclonal Antibody Thereof
10 <130> FILE REFERENCE: 2004-1597A/WMC/00279
12 <140> CURRENT APPLICATION NUMBER: 10/509,073C
13 <141> CURRENT FILING DATE: 2005-01-12
15 <160> NUMBER OF SEQ ID NOS: 22
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 1395
19 <212> TYPE: DNA
20 <213> ORGANISM: Homo sapiens
22 <400> SEQUENCE: 1
23 atg cca aag aaa gca aag cct aca ggg agt ggg aag gaa gag ggg ccg   48
24 Met Pro Lys Lys Ala Lys Pro Thr Gly Ser Gly Lys Glu Gly Pro
25           5           10           15
27 gct ccc tgt aag cag atg aag tta gaa gca gct ggg ggg cct tca gct   96
28 Ala Pro Cys Lys Gln Met Lys leu Glu Ala Ala Gly Gly Pro Ser Ala
29           20           25           30
31 tta aac ttt gac agt ccc agt agt ctc ttt gaa agt tta atc tcg ccc   144
32 Leu Asn Phe Asp Ser Pro Ser Ser Leu Phe Glu Ser Leu Ile Ser Pro
33           35           40           45
35 atc aag aca gag act ttt ttc aag gaa ttc tgg gag cag aag ccc ctt   192
36 Ile Lys Thr Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu
37           50           55           60
39 ctc att cag aga gat gac cct gca ctg gcc aca tac tat ggg tcc ctg   240
40 Leu Ile Gln Arg Asp Asp Pro Ala Leu Ala Thr Tyr Tyr Gly Ser Leu
41   65           70           75           80
43 ttc aag cta aca gat ctg aag agt ctg tgc agc cgg ggg atg tac tat   288
44 Phe Lys Leu Thr Asp Leu Lys Ser Leu Cys Ser Arg Gly Met Tyr Tyr
45           85           90           95
47 gga aga gat gtg aat gtc tgc cgg tgt gtc aat ggg aag aag aag gtt   336
48 Gly Arg Asp Val Asn Val Cys Arg Cys Val Asn Gly Lys Lys Lys Val
49           100          105          110
51 tta aat aaa gat ggc aaa gca cac ttt ctt cag ctg aga aaa gat ttt   384
52 Leu Asn Lys Asp Gly Lys Ala His Phe Leu Gln Leu Arg Lys Asp Phe
53           115          120          125
55 gat cag aaa agg gca acg att cag ttt cac caa cct cag aga ttt aag   432
56 Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
57           130          135          140
59 gat gag ctt tgg agg atc cag gag aag ctg gaa tgt tac ttt ggc tcc   480
60 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser
61 145          150          155          160

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63 ttg gtt ggc tcg aat gtg tac ata act ccc gca gga tct cag ggc ctg 528
64 Leu Val Gly Ser Asn Val Tyr Ile Thr Pro Ala Gly Ser Gln Gly Leu
65 165 170 175
67 ccg ccc cat tat gat gat gtc gag gtt ttc atc ctg cag ctg gag gga 576
68 Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly
69 180 185 190
71 gag aaa cac tgg cgc ctc tac cac ccc act gtg ccc ctg gca cga gag 624
72 Glu Lys His Trp Arg Leu Tyr His Pro Thr Val Pro Leu Ala Arg Glu
73 195 200 205
75 tac agc gtg gag gcc gag gaa agg atc ggc agg ccg gtg cat gag ttt 672
76 Tyr Ser Val Glu Ala Glu Glu Arg Ile Gly Arg Pro Val His Glu Phe
77 210 215 220
79 atg ctg aag ccg ggt gat ttg ttg tac ttt ccc aga gga acc att cat 720
80 Met Leu Lys Pro Gly Asp Leu Leu Tyr Phe Pro Arg Gly Thr Ile His
81 225 230 235 240
83 caa gcg gac act cct gcg ggg ctg gcc cac tcg act cac gtg acc atc 768
84 Glu Ala Asp Thr Pro Ala Gly Leu Ala His Ser Thr His Val Thr Ile
85 245 250 255
87 agc acc tac cag aac aat tca tgg gga gat ttc ctt ttg gat acc atc 816
88 Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Phe Leu Leu Asp Thr Ile
89 260 265 270
91 tcg ggg ctt gta ttt gat act gca aag gaa gac gtg gag tta cgg acc 864
92 Ser Gly Leu Val Phe Asp Thr Ala Lys Glu Asp Val Glu Leu Arg Thr
93 275 280 285
95 ggc ata ccc cgg cag ctg ctc ctg gtg gaa tcc aca act gtt gct aca 912
96 Gly Ile Pro Arg Gln Leu Leu Leu Val Glu Ser Thr Thr Val Ala Thr
97 290 295 300
99 aga cga tta agt ggc ttc ctg agg aca ctt gca gac cgg ctg gag ggc 960
100 Arg Arg Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Arg Leu Glu Gly
101 305 310 315 320
103 acc aaa gaa ctg ctt tcc tca gac atg aag aag gat ttt att atg cac 1008
104 Thr Lys Glu Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Ile Met His
105 325 330 335
107 aga ctc ccc cct tac tct gcg gga gat ggg gca gag ctg tca aca cca 1056
108 Arg Leu Pro Pro Tyr Ser Ala Gly Asp Gly Ala Glu Leu Ser Thr Pro
109 340 345 350
111 ggt gga aag tta ccg agg ctg gac agt gta gtg aga ctg cag ttt aaa 1104
112 Gly Gly Lys Leu Pro Arg Leu Asp Ser Val Val Arg Leu gln Phe Lys
113 355 360 365
115 gac cac att gtc ctc aca gta ctg ccg gat caa gat caa tct gat gaa 1152
116 Asp His Ile Val Leu Thr Val Leu Pro Asp Gln Asp Gln Ser Asp Glu
117 370 375 380
119 gct caa gaa aag atg gtg tac atc tat cat tcc tta aag aat agt aga 1200
120 Ala Gln Glu Lys Met Val Tyr Ile Tyr His Ser Leu Lys Asn Ser Arg
121 385 390 395 400
123 gag aca cac atg atg gga aat gag gag gaa aca gag ttt cat gga ctt 1248
124 Glu Thr His Met Met Gly Asn Glu Glu Glu Thr Glu Phe His Gly Leu
125 405 410 415
127 cgc ttc cct ttg tca cat ttg gat gca ctg aag caa att tgg aat agt 1296

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128 Arg Phe Pro Leu Ser His Leu Asp Ala Leu Lys Gln Ile Trp Asn Ser
129          420          425          430
131 cca gct att tct gtc aag gac ctg aaa ctt act aca gat gag gaa aag 1344
132 Pro Ala Ile Ser Val Lys Asp Leu Lys Leu Thr Thr Asp Glu Glu Lys
133          435          440          445
135 gaa agc ctg gta tta tcc ctc tgg aca gaa tgt tta att caa gta gtc 1392
136 Glu Ser Leu Val Leu Ser Leu Trp Thr Glu Cys Leu Ile Gln Val Val
137          450          455          460
139 tag 1395
142 <210> SEQ ID NO: 2
143 <211> LENGTH: 1398
144 <212> TYPE: DNA
145 <213> ORGANISM: Mus musculus
147 <400> SEQUENCE: 2
148 atg cca aag aaa gtg cag ccc aca ggg gat gag aac gaa gaa gag tct 48
149 Met Pro Lys Lys Val Gln Pro Thr Gly Asp Glu Asn Glu Glu Glu Ser
150          5          10          15
152 gtt cct tgc aag cgg gtg aag gag gag ctg cct gaa acg ctt tct gta 96
153 Val Pro Cys Lys Arg Val Lys Glu Glu Leu Pro Glu Thr Leu Ser Val
154          20          25          30
156 tta aac ttt gac agc ccc agt agt ttc ttc gaa agt tta atc tca ccc 144
157 Leu Asn Phe Asp Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro
158          35          40          45
160 atc aaa gta gag act ttt ttc aag gaa ttc tgg gaa caa aag ccc ctt 192
161 Ile Lys Val Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu
162          50          55          60
164 ctc att cag agg gat gac cct gta ctg gcc aaa tat tac cag tct ctg 240
165 Leu Ile Gln Arg Asp Asp Pro Val Leu Ala Lys Tyr Tyr Gln Ser Leu
166          65          70          75          80
168 ttc agc ctc tca gat ctg aag aga ctc tgc aag aaa gga gtg tac tat 288
169 Phe Ser Leu Ser Asp Leu Lys Arg Leu Cys Lys Lys Gly Val Tyr Tyr
170          85          90          95
172 gga aga gac gtg aat gtc tgc cgg agc atc agt ggg aag aag aag gtt 336
173 Gly Arg Asp Val Asn Val Cys Arg Ser Ile Ser Gly Lys Lys Lys Val
174          100          105          110
176 tta aat aag gat ggc aga gca cat ttt ctt cag ctg aga aaa gat ttt 384
177 Leu Asn Lys Asp Gly Arg Ala His Phe Leu Gln Leu Arg Lys Asp Phe
178          115          120          125
180 gat cag aag agg gca aca att cag ttt cac caa cct cag aga tat aag 432
181 Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Tyr Lys
182          130          135          140
184 gat gag ctg tgg cgg atc cag gaa aag ctg gaa tgt tac ttt ggg tcc 480
185 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser
186          145          150          155          160
188 tta gta ggc tgc aat gtg tac atg act cct gca gga tct cag ggc ctc 528
189 Leu Val Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu
190          165          170          175
192 cct cca cat tat gat gat gtt gag gtt ttt atc ctg cag ctg gag gga 576
193 Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly

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194          180          185          190
196 acg aaa cac tgg cgc ctg tac tcc cca act gtg ccc ctg gca cac gag 624
197 Thr Lys His Trp Arg Leu Tyr Ser Pro Thr Val Pro Leu Ala His Glu
198          195          200          205
200 tac agt gtg gaa tct gag gac cgg atc ggc aca ccg aca cac gac ttc 672
201 Tyr Ser Val Glu Ser Glu Asp Arg Ile Gly Thr Pro Thr His Asp Phe
202          210          215          220
204 ctg ctg aag cct gga gat ttg ttg tac ttt ccc aga ggg acc att cat 720
205 Leu Leu Lys Pro Gly Asp Leu Leu Tyr Phe Pro Arg Gly Thr Ile His
206 225          230          235          240
208 cag gca gaa act cct tca ggc ctg gcc tac tct att cac ctg act att 768
209 Gln Ala Glu Thr Pro Ser Gly Leu Ala Tyr Ser Ile His Leu Thr Ile
210          245          250          255
212 agc acc tac cag aac aat tca tgg gga gac tgc ctt ttg gat tcc att 816
213 Ser Thr Tyr Gln Asn Asn Ser Trp Gly Asp Cys Leu Leu Asp Ser Ile
214          260          265          270
216 tcg ggg ttc gta ttt gac att gca aag gaa gat gtg gca tta agg agt 864
217 Ser Gly Phe Val Phe Asp Ile Ala Lys Glu Asp Val Ala Leu Arg Ser
218          275          280          285
220 gga atg ccc cgg cgg atg ctc ctg aat gtg gaa acc cca gct gat gta 912
221 Gly Met Pro Arg Arg Met Leu Leu Asn Val Glu Thr Pro Ala Asp Val
222          290          295          300
224 aca agg aag ttg agt ggc ttt ctg agg act ctt gca gac cag ctc gag 960
225 Thr Arg Lys Leu Ser Gly Phe Leu Arg Thr Leu Ala Asp Gln Leu Glu
226 305          310          315          320
228 ggc aga gaa gag ctg ctg tca tca gat atg aag aag gac ttc gtc aag 1008
229 Gly Arg Glu Glu Leu Leu Ser Ser Asp Met Lys Lys Asp Phe Val Lys
230          325          330          335
232 cac aga ctc cct cct ttc ttc gag gga aat gga acg gag acg atg gac 1056
233 His Arg Leu Pro Pro Phe Phe Glu Gly Asn Gly Thr Glu Thr Met Asp
234          340          345          350
236 cca ggt aaa cag ttg cca agg ttg gac aac ata ata aga ctg cag ttc 1104
237 Pro Gly Lys Gln Leu Pro Arg Leu Asp Asn Ile Ile Arg Leu Gln Phe
238          355          360          365
240 aaa gat cac att gtc ctc aca gta ggg cca gat aag aat cca ttt gat 1152
241 Lys Asp His Ile Val Leu Thr Val Gly Pro Asp Lys Asn Pro Phe Asp
242          370          375          380
244 gaa gct caa caa aag gtg gtt tac atc tat cat tct ctg aag aat gtg 1200
245 Glu Ala Gln Gln Lys Val Val Tyr Ile Tyr His Ser Leu Lys Asn Val
246 385          390          395          400
248 agg cag atg cac atg ata gga gaa gag gag gaa tcc gag att ttc ggt 1248
249 Arg Gln Met His Met Ile Gly Glu Glu Glu Ser Glu Ile Phe Gly
250          405          410          415
252 ctt cgc ttt cct tta tca cat gtg gat gct ctg aag caa atc tgg tgc 1296
253 Leu Arg Phe Pro Leu Ser His Val Asp Ala Leu Lys Gln Ile Trp Cys
254          420          425          430
256 ggg tca cca att cgt gtt aag gaa ctg aaa ctt gac aca gat gaa gaa 1344
257 Gly Ser Pro Ile Arg Val Lys Glu Leu Lys Leu Asp Thr Asp Glu Glu
258          435          440          445

```

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260 aag gag aac ctg gca ctg tct ctc tgg tcg gag tct tta atc caa gta 1392
261 Lys Glu Asn Leu Ala Leu Ser Leu Trp Ser Glu Ser Leu Ile Gln Val
262 450 455 460
263 ctc tag 1398
264 Leu
265 465
268 <210> SEQ ID NO: 3
269 <211> LENGTH: 1398
270 <212> TYPE: DNA
271 <213> ORGANISM: Rattus norvegicus
273 <400> SEQUENCE: 3
274 atg cca aag aaa gtg aag ccc aca ggg gat gag aat gaa gaa gag tct 48
275 Met Pro Lys Lys Val Lys Pro Thr Gly Asp Glu Asn Glu Glu Glu Ser
276 5 10 15
278 gtt cct tgc aag cag gtg aaa gag gag cta cct aat acg ctt tct gta 96
279 Val Pro Cys Lys Gln Val Lys Glu Glu Leu Pro Asn Thr Leu Ser Val
280 20 25 30
282 tta aac ttt gac agc ccc agt agt ttc ttt gaa agt tta ata tca ccc 144
283 Leu Asn Phe Asp Ser Pro Ser Ser Phe Phe Glu Ser Leu Ile Ser Pro
284 35 40 45
286 atc aaa gta gag aca ttt ttc aag gaa ttc tgg gaa cag aag ccc ctt 192
287 Ile Lys Val Glu Thr Phe Phe Lys Glu Phe Trp Glu Gln Lys Pro Leu
288 50 55 60
290 ctc att cag aga gat gac cct tcg ctg gcc gca tat tac cag tct ctg 240
291 Leu Ile Gln Arg Asp Asp Pro Ser Leu Ala Ala Tyr Tyr Gln Ser Leu
292 65 70 75 80
294 ttc agc ctc tca gat ctg agg agt ctc tgc agc caa ggg ctg tac tat 288
295 Phe Ser Leu Ser Asp Leu Arg Ser Leu Cys Ser Gln Gly Leu Tyr Tyr
296 85 90 95
298 gga aga gat gtc aat gtc tgc cgg tgc atc ggt ggg aag aag aag gtt 336
299 Gly Arg Asp Val Asn Val Cys Arg Cys Ile Gly Gly Lys Lys Lys Val
300 100 105 110
302 tta aat aag gat ggc aaa gca cag ttt ctt cag ctg aga aaa gat ttt 384
303 Leu Asn Lys Asp Gly Lys Ala Gln Phe Leu Gln Leu Arg Lys Asp Phe
304 115 120 125
306 gat cag aag agg gca aca att cag ttt cat cag cca cag aga ttt aag 432
307 Asp Gln Lys Arg Ala Thr Ile Gln Phe His Gln Pro Gln Arg Phe Lys
308 130 135 140
310 gat gag ctc tgg agg atc cag gaa aag ctg gaa tgt tac ttt ggc tcc 480
311 Asp Glu Leu Trp Arg Ile Gln Glu Lys Leu Glu Cys Tyr Phe Gly Ser
312 145 150 155 160
314 tta gta ggc tca aat gtg tac atg act ccc gca gga tct cag ggc ctt 528
315 Leu Val Gly Ser Asn Val Tyr Met Thr Pro Ala Gly Ser Gln Gly Leu
316 165 170 175
318 cct cca cat tac gac gat gtt gag gtt ttt atc ctg cag ctg gag gga 576
319 Pro Pro His Tyr Asp Asp Val Glu Val Phe Ile Leu Gln Leu Glu Gly
320 180 185 190
322 agg aaa cgt tgg cgc ctg tac tcc cca act gtg ccc ctg gcg cgt gag 624
323 Arg Lys Arg Trp Arg Leu Tyr Ser Pro Thr Val Pro Leu Ala Arg Glu

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/10/509,073C

DATE: 04/16/2007
TIME: 18:45:58

Input Set : A:\Tsuneoka 2004_1597A.txt
Output Set: N:\CRF4\04162007\J509073C.raw

Invalid Line Length:

The rules require that a line not exceed 72 characters in length. This includes spaces.

Seq#:2; Line(s) 170,190

Seq#:3; Line(s) 356

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22

VERIFICATION SUMMARY

DATE: 04/16/2007

PATENT APPLICATION: US/10/509,073C

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